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TO: James Schultz
Location: rem/2d18/2c18
Art Unit: 1635
Friday, September 17, 2004
Case Serial Number: 10/019595

From: Paul Schulwitz
Location: Biotech-Chem Library
REM-1A65
Phone: (571)272-2527

paul.schulwitz@uspto.gov

Search Notes

Examiner Schultz,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Paul Schulwitz
Technical Information Specialist
STIC Biotech/Chem Library
(571)272-2527

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131947

—MEY

From: Schultz, James
Sent: Wednesday, September 08, 2004 1:49 PM
To: STIC-Biotech/ChemLib
Subject: Seq Search 10/019,595

Hello,
Could you please run a length limited nucleotide sequence search on SEQ ID NO: 1 in the above entitled case which returns hits 30 nucleotides long and under?

Thanks,
Doug Schultz

James Douglas Schultz, PhD

AU 1635 (Biotechnology)
Patent Examiner
United States Patent and Trademark Office
(Office) REM 2D18
(Mail) REM 2C18
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Searcher Prep/Rev. Time: _____

Type of Search

NA Sequence: #

AA Sequence :#

Structure: # _____

Bibliographic:

Litigation:

Patent Family:

Other:

Vendors and cost where applicable

STN: _____

DIALOG: _____

QUESTEL/ORBIT: _____

LEXIS/NEXIS: _____

SEQUENCE SYSTEM:

WWW/Internet:

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DEFINITION Sequence 7 from Patent WO0071747.

ACCESSION AX048408
VERSION 1 GI:12225572

KEYWORDS synthetic construct

SOURCE synthetic construct

ORGANISM artificial sequences.

REFERENCE Boekenkamp,D., Hoppe,H.U. and Burgstaller,P.

AUTHORS Production and use of the same

JOURNAL Patent: WO 0071747-A 7 30-NOV-2000;

FEATURES Aventis Research & Technologies GmbH & Co. KG (DE)

source Location/Qualifiers

1. .29 /organism="synthetic construct"
 /mol type="unassigned DNA"
 /db Xref="taxon:32630"
 /note="Region A"

ORIGIN

Query Match 0.5%; Score 24.4; DB 6; Length 29;
 Best Local Similarity 96.2%; Pred. No. 2.2e+06;
 Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5188 AACAAAGAAAAAAGAAAAAAACC 5213
 Db 26 AAAAAGAAAAAAGAAAAAAACC 1

RESULT 7
 AX048409
 LOCUS AX048409
 DEFINITION Sequence 8 from Patent WO0071747.
 ACCESSION AX048409
 VERSION GI:12225573
 KEYWORDS synthetic construct

SOURCE synthetic construct

ORGANISM artificial sequences.

REFERENCE Boekenkamp,D., Hoppe,H.U. and Burgstaller,P.

AUTHORS Detection system for separating constituents of a sample and production and use of the same

JOURNAL Patent: WO 0071747-A 8 30-NOV-2000;

FEATURES Aventis Research & Technologies GmbH & Co. KG (DE)

source Location/Qualifiers

1. .29 /organism="synthetic construct"
 /mol type="unassigned DNA"
 /db Xref="taxon:32630"
 /note="Linker"

ORIGIN

Query Match 0.5%; Score 24.4; DB 6; Length 29;
 Best Local Similarity 96.2%; Pred. No. 2.2e+06;
 Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5188 AACAAAGAAAAAAGAAAAAAACC 5213
 Db 4 AAAAAGAAAAAAGAAAAAAACC 29

RESULT 8
 AX052994
 LOCUS AX052994
 DEFINITION Sequence 10 from Patent WO0071749.
 ACCESSION AX052994
 VERSION GI:12227096
 KEYWORDS synthetic construct

SOURCE synthetic construct

ORGANISM artificial sequences.

REFERENCE 1 Boekenkamp,D., Hoppe,H.U., Burgstaller,P., Konz,D., Woelk,U. and Pignot,M.

AUTHORS Detection system for analyzing molecular interactions, production and utilization thereof and utilization thereof

JOURNAL Patent: WO 0071749-A 10 30-NOV-2000;

FEATURES Location/Qualifiers

1. .29 /organism="synthetic construct"
 /mol type="unassigned DNA"
 /db Xref="taxon:32630"
 /note="Beschreibung der kunstlichen Sequenz: Puromycin-Linker"

ORIGIN

Query Match 0.5%; Score 24.4; DB 6; Length 29;
 Best Local Similarity 96.2%; Pred. No. 2.2e+06;
 Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5188 AACAAAGAAAAAAGAAAAAAACC 5213
 Db 4 AAAAAGAAAAAAGAAAAAAACC 29

RESULT 9
 AX353685
 LOCUS AX353685
 DEFINITION Sequence 5 from Patent WO0204656.
 ACCESSION AX353685
 VERSION AX353685.1 GI:18618749

KEYWORDS synthetic construct

SOURCE synthetic construct

ORGANISM synthetic construct

REFERENCE 1 Wagner,P. and Polakowski,T.

AUTHORS Bio-probes and use thereof

JOURNAL Patent: WO 0204656-A 5 17-JAN-2002;

FEATURES Xzillion GmbH & Co.KG (DE)

source Location/Qualifiers

1. .29 /organism="synthetic construct"
 /mol type="unassigned DNA"
 /db Xref="taxon:32630"
 /note="Linker mit Puromycin am 3'-Ende"

ORIGIN

Query Match 0.5%; Score 24.4; DB 6; Length 29;
 Best Local Similarity 96.2%; Pred. No. 2.2e+06;
 Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5188 AACAAAGAAAAAAGAAAAAAACC 5213
 Db 4 AAAAAGAAAAAAGAAAAAAACC 29

RESULT 10
 AX662302
 LOCUS AX662302
 DEFINITION Sequence 41 from Patent WO02059293.
 ACCESSION AX662302
 VERSION AX662302.1 GI:29163186

KEYWORDS synthetic construct

SOURCE synthetic construct

ORGANISM synthetic construct

REFERENCE 1 Forster,A.C. and Blacklow,S.C.

AUTHORS Process and compositions for peptide, protein and peptidomimetic synthesis

JOURNAL Patent: WO 02059293-A 41 01-AUG-2002;

Forster, Anthony C. (US) ; Blacklow, Stephen C. (US)

FEATURES source	Location/Qualifiers 1 .29 /organism="synthetic construct" /mol_type="unassigned DNA" /db_xref="taxon:32630" /note="FROM SYNTHETIC DNA"	ORIGIN	TITLE Convergent synthesis of branched and multiply connected macromolecular structures JOURNAL Patent: US 5830658-A 12-03-NOV-1998; FEATURES Location/Qualifiers source 1 .30 /organism="unknown" /mol_type="unassigned DNA"
Query Match Best Local Similarity 96.2%; Pred. No. 2.2e+06; Length 29; Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	Qy 5188 AACAAAAAAAGAAAAAAAC 5213 Db 4 AAAAAGAAAAAAAGAAAAAC 29	ORIGIN	TITLE Query Match 0 .5%; Score 24.2%; DB 6; Length 30; JOURNAL Best Local Similarity 89.7%; Pred. No. 2.4e+06; FEATURES Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0; source 1 .30 /organism="unknown" /mol_type="unassigned DNA"
RESULT 11 BD04968	BD204968 29 bp DNA linear PAT 17-JUL-2003	RESULT 13 AR127791	TITLE Query Match 0 .5%; Score 24.2%; DB 6; Length 30; JOURNAL Sequence 12 from patent US 6180777. FEATURES ACCESSION AR127791 VERSION AR127791.1 GI:14114386 KEYWORDS SOURCE Unknown ORGANISM Unknown REFERENCE 1 (bases 1 to 30) AUTHORS Horn,T. TITLE Synthesis of branched nucleic acids JOURNAL Patent: US 6180777-A 12-30-JUN-2001; FEATURES Location/Qualifiers source 1 .30 /organism="unknown" /mol_type="unassigned DNA"
REFERENCE AUTHORS Kuijmelis,R.G. and Wagner,R. TITLE Protein array enabling site specification JOURNAL Patent: JP 2002310505-A 3 09-APR-2002; COMMENT PHYLOS INC COMMENT Artificial Sequence FN JP 2002510505-A/3 FD 09-APR-2002 FR 31-MAR-1999 JP 2000542484 FR 03-APR-1998 US 60/080686 PI ROBERT G KUIJMELIS RICHARD WAGNER PC C12N15/09,C07H21/02,C07H21/04,C12M1/00,C12Q1/68,G01N33/566, PC G01N33/68, PC C12N15/00 CC Oligonucleotide used for attaching puromycin FH Key FT Location/Qualifiers source 1 .29 /organism="Artificial Sequence". FT Location/Qualifiers source 1 .29 /organism="synthetic construct" /mol_type="genomic DNA" /db_xref="taxon:32630"	Qy 5183 CTCTAACACAAAAAAAGAAAAAA 5211 Db 1 CACACAAAAAAAGAAAAAAAGAAA 29	ORIGIN	TITLE Query Match 0 .5%; Score 24.2%; DB 6; Length 30; JOURNAL Best Local Similarity 89.7%; Pred. No. 2.4e+06; FEATURES Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0; source 1 .30 /organism="unknown" /mol_type="unassigned DNA"
RESULT 14 I28373	I28373 30 bp DNA linear PAT 06-FEB-1997	RESULT 14 I28373	TITLE Query Match 0 .5%; Score 24.2%; DB 6; Length 30; JOURNAL Sequence 12 from patent US 5571677. FEATURES ACCESSION I28373 VERSION I28373.1 GI:1819149 KEYWORDS SOURCE Unknown ORGANISM Unknown REFERENCE 1 (bases 1 to 30) AUTHORS Gryaznov,S.M. TITLE Convergent synthesis of branched and multiply connected macromolecular structures JOURNAL Patent: US 5571677-A 12-05-NOV-1996; FEATURES Location/Qualifiers source 1 .30 /organism="unknown" /mol_type="unassigned DNA"
FEATURES source	Query Match Best Local Similarity 96.2%; Pred. No. 2.2e+06; Length 29; Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	ORIGIN	TITLE Query Match 0 .5%; Score 24.2%; DB 6; Length 30; JOURNAL Best Local Similarity 89.7%; Pred. No. 2.4e+06; FEATURES Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
RESULT 12 AR05144	AR051244 Sequence 12 from patent US 5830658. DNA linear PAT 29-SEP-1999	RESULT 12 AR05144	TITLE Query Match 0 .5%; Score 24.2%; DB 6; Length 30; JOURNAL Sequence 12 from patent US 5830658. FEATURES ACCESSION AR051244 KEYWORDS SOURCE Unknown ORGANISM Unknown REFERENCE 1 (bases 1 to 30) AUTHORS Gryaznov,S.M.

Db 1 CAGACAAAAAA...AAAAAAA 29

RESULT 15
AR009472/C AR009472 Sequence 22 from Patent US 5756295. linear PAT 04-DEC-1998
LOCUS Definition 24 bp DNA
DEFINITION Sequence 22 from Patent US 5756295.
ACCESSION AR009472
VERSION AR009472.1 GI:3968277
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 24)
AUTHORS Onda, H. and Hosoya, M.
TITLE DNA Primer and a method for screening DNAs
JOURNAL Patent: US 5756295-A 22 26-VAY-1998;
FEATURES Location/Qualifiers
FEATURES 1..24
source /organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Query Match 0.5%; Score 24; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5212 CCATGGTACCCGGATCCCTCGAATT 5235
Db 24 CCATGGTACCCGGATCCCTCGAATT 1

Search completed: September 15, 2004, 22:19:07
Job time : 19500 secs

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CC range of (I), e.g. diagnostic or pharmaceutical agents, secondary
 CC metabolites, herbicides or pesticides. (A) allow simultaneous, parallel
 CC detection of many different analytes (high throughput capacity),
 CC relatively simply (only a few incubation and washing steps are required)
 CC and with high sensitivity and selectivity. This sequence represents
 CC primer used in the amplification of the c-myc DNA fragment which encodes
 CC an epitope used to illustrate the method of the invention
 XX Sequence 29 BP; 27 A; 2 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.5%; Score 24.4; DB 6;
 Best Local Similarity 96.2%; Pred. No. 8.6e+04; Length 29;
 Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 SQ

QY 5188 AACAAAAAAAGAAAAAAACC 5213
 Db 4 AAAAAGAAAAAAAGAAAAACC 29

RESULT 4

AAK98637 standard; DNA; 29 BP.

XX AAK98637;

XX DT 19-APR-2002 (first entry)

DE S cerevisiae alpha factor receptor STE2 vector linker.

XX Biological material detection; electrophoresis; bioprobe isolation;

KW alpha factor receptor; STE2; linker; ss.

XX Synthetic.

XX Key FH 19 Location/Qualifiers

XX FT modified_base 29 /*tag= a

FT /mod_base= OTHER

FT /note= "modified by puromycin"

PN WO200204656-A2.

XX PD 17-JAN-2002.

XX DR 26-JUN-2001; 2001WO-EP007259.

XX PT 07-JUL-2000; 2000DE-01033194.

XX PA (XZL1-) XZILLION GMBH & CO KG.

XX PI Wagner P, Polakowski T;

XX DR 2002-154934/20.

XX Detecting and purifying biological material by (di)electrophoresis, which comprises
 PT useful e.g. for separating tissues and viruses, comprises using a probe
 PT that alters (di)electrophoretic properties.
 XX PS Example 1; Page 12; 20P; German.
 XX The present invention relates to a method for the detection or
 CC purification of biological material by electrophoresis, which comprises
 CC (i) treating the biological material containing different species with a
 CC bioprobe and (ii) establishing an electric field for detection or
 CC purification of at least one complex formed between the biological
 CC material being tested and a specifically bound bioprobe. The method is
 CC used for detection and purification of tissue, cells, cell organelles,
 CC viruses, proteins, nucleic acids, lipids and/or other organic compounds.
 CC It can also be used for the isolation of specific bioprobes from a
 CC library of bioprobes. The present sequence is a linker described in the
 CC exemplification of the invention
 XX Sequence 29 BP; 27 A; 2 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.5%; Score 24.4; DB 6;
 Best Local Similarity 96.2%; Pred. No. 8.6e+04; Length 29;
 Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 SQ

QY 5188 AACAAAAAAAGAAAAACC 5213
 Db 4 AAAAAGAAAAAAAGAAAAACC 29

RESULT 5

AAV48087 standard; DNA; 30 BP.

XX ID AAV48087;
 XX AC AAV48087;
 XX DT 27-OCT-1998 (first entry)
 XX DE Oligonucleotide 30-P.
 XX FN In situ translation; RNA-protein fusion; binding reagent; antibody;
 XX KW industrial catalyst; ss.
 XX OS Synthetic.
 XX Key FH In situ translation; RNA-protein fusion; binding reagent; antibody;
 XX FT modified_base 30 /*tag= a
 FT /note= "Puromycin"
 XX PN WO9831700-A1.
 XX Key FH In situ translation; RNA-protein fusion; binding reagent; antibody;
 XX FT modified_base 30 /*tag= a
 FT /note= "Puromycin"
 XX PN WO9831700-A1.
 XX PD 23-JUL-1998.
 XX PR 14-JAN-1998;
 XX PR 21-JAN-1997;
 XX PR 06-NOV-1997;
 XX PR 06-NOV-1997;
 XX PA (GEHO) GEN HOSPITAL CORP.
 XX PI Szostak JW, Roberts RW, Liu R;
 XX DR WPI; 1998-414032/35.
 XX PT Selection of specific Protein by screening protein-RNA fusions generated
 PT in vitro or in situ - useful for, e.g. identifying enzymes and antibodies
 PT with altered properties, potentially useful as catalysts or for therapy
 PT or diagnosis.
 XX PS Disclosure; Page 39; 94P; English.

XX The Oligonucleotides AAV48087, AAV48089-V48091 and AAV48096-V48098 and
 CC variations were used to generate RNA-protein fusions. These were used in
 CC the selection of a specific protein or RNA, by in vitro or in situ
 CC translation of candidate RNA molecules to produce RNA-protein fusions,
 CC then selecting specific RNA protein fusions. The method is used to select
 CC proteins (or DNA encoding them) having altered properties, e.g. for
 CC identification of new binding reagents, to identify improved human
 CC antibodies or new enzymes. These proteins are potentially useful in
 CC diagnosis and therapy, or as industrial catalysts. The methods allow many
 CC rounds of selection and amplification to be performed, resulting in
 CC enrichment of even very rare molecules and allowing isolation of proteins
 CC that bind specifically to almost any compound or catalyse almost any
 CC reaction
 XX Sequence 30 BP; 27 A; 2 C; 0 G; 0 T; 0 U; 1 Other;

Query Match 0.5%; Score 24.4; DB 2;
 Best Local Similarity 96.2%; Pred. No. 8.8e+04;
 Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 SQ

QY 5188 AACAAAAAAAGAAAAACC 5213

Db	4 AAAAATTTTAAATTTTAAATTTTAAACCC 29	ID AAF60462 standard; DNA; 30 BP. XX XX AC AAF60462; XX DT 27-APR-2001 (first entry) XX DE Oligonucleotide Clamp #22. XX KW Oligonucleotide clamp; ds. XX OS Unidentified.
RESULT 6		
AAQ83940		
ID AAQ83940	standard; DNA; 30 BP.	
XX		
AC AAQ83940;		
XX	25-MAR-2003 (revised)	
DT	04-OCT-1995 (first entry)	
XX	Oligonucleotide clamp o, for producing comb-type branched polymer.	
XX	HIV; pol; nef; oligonucleotide clamp; branched; macromolecule; ss.	
XX	Synthetic.	
XX	Location/Qualifiers	
PR		
FT modified_base 1 /*tag= a		
FT /note= "Modified with SP(O-)- (=O)-"		
PT PI		
XX	WO9501365-A1.	
XX	DR WPI; 2001-201911/20.	
PD 12-JAN-1995.		
XX	PT Synthesizing branched nucleic acids useful as diagnostic and molecular probes, involves combining first units having haloalkylamino groups and second units having thiol or phosphorothioate groups.	
PF 05-JUL-1994;		
XX	PT Example 8; Col 19; 20PP; English.	
PR 02-JUL-1993;		
XX	XX The present invention relates to a method for synthesising a branched or multiply connected macromolecular structure, comprising Oligonucleotide clamps (OC). The macromolecular structure is capable of specifically binding to a target molecule, and can therefore be used as probes. At least one OC comprises a target binding sequence that binds specifically and stably with the target molecule, and at least two OCs comprise signal generation moieties capable of generating a detectable signal in the presence of the target molecule. In addition the OCs are connected to one another by thiaoxylanine, or thiophosphorylaminobridges. The present sequence is an OC used in the present invention	
PA (LYNX-) LYNX THERAPEUTICS INC.		
XX	CC Sequence 30 BP; 27 A; 3 C; 0 G; 0 T; 0 U; 0 Other;	
PI Gryaznov SM;		
XX	CC Query Match 0.5%; Score 24.2; DB 04;	
DR 1995-060944/08.		
XX	CC Best Local Similarity 89.7%; Pred. No. 9.7e+03; Indels 0; Gaps 0;	
PT Synthesis of branched polymers and novel branched polymeric structures -		
XX	CC Matches 26; Conservative 0; Mismatches 3;	
PT used as molecular probes esp. for detecting poly-nucleotide(s).		
XX	CC Example 8; Page 33; 52PP; English.	
PS		
XX	CC The sequences Given in AAQ83938, AAQ83952 and AAQ83940 are used in the construction of an oligonucleotide clamp. The clamp is a comb-type branched polymer which has 3' termini and was used to bind a target sequence comprising a segment of the HIV pol and nef genes in single stranded or double stranded forms. An oligonucleotide clamp is a compound capable of forming a covalently closed macrocycle or a stable circular complex after specifically binding to the target polynucleotide.	
XX	CC Oligonucleotide clamps generally comprise one or more oligonucleotide moieties capable of specific binding to the target molecule and one or more pairs of binding moieties covalently linked to the Oligonucleotide moieties. Upon annealing of the oligonucleotides moieties to the target polynucleotide, the binding moieties of a pair are brought into juxtaposition so that they form a stable covalent or non-covalent linkage or complex. The interaction of the binding moieties effectively clamps the specifically annealed oligonucleotide moieties to the target polynucleotide. (Updated on 25-MAR-2003 to correct PN field.)	
XX	CC Sequence 30 BP; 27 A; 3 C; 0 G; 0 T; 0 U; 0 Other;	
SQ		
XX	CC Query Match 0.5%; Score 24.2; DB 2;	
XX	Best Local Similarity 89.7%; Pred. No. 9.7e+04; Indels 0; Gaps 0;	
XX	CC Matches 26; Conservative 0; Mismatches 3;	
XX	XX AAQ50581;	
AC AAQ50581;		
XX	XX DT 25-MAR-2003 (revised)	
XX	XX DT 24-MAY-1994 (first entry)	
XX	XX DE Asparaginylendopeptidase Oligonucleotide	
XX	XX KW Asparaginylendopeptidase; Canavalia ensiformis; seed; L-asparagine; primer; PCR; protein fragmentation; peptide synthesis; ss.	
OS		
XX	XX Synthetic.	
XX	XX PN JP0526960-A.	
PD 26-OCT-1993.		
RESULT 7		
AAFP60462		

XX 07-AUG-1992; 92JP-00231602.
 PF XX 07-FEB-1992; 92JP-00056023.
 PR PA (TAKI) TAKARA SHUZO CO LTD.
 XX DR; 1993-373587/47.
 XX New gene for encoding asparaginyl endo-peptidase - comprises 8 specified
 PT DNA sequences.
 XX Disclosure; Page 29; 35pp; Japanese.
 XX A gene encoding asparaginylendopeptidase is claimed. 8 DNA sequences are
 CC given (AAQ5059-66). The enzyme is a protease derived from a seed of
 CC Canavalia ensiformis which selectively hydrolyses C-terminal amide bond
 CC of L-asparagine residue (see AAR4303 and AAR4304). The enzyme is useful
 CC for protein fragmentation and enzymatic peptide synthesis. The primers
 CC given in AAQ50567-68 AAQ50576-77 and AAQ50583-90 were used in the
 CC isolation of the fragments given in AAQ50569-75 and AAQ50578-79, by PCR.
 CC (Updated on 25-MAR-2003 to correct PA field.)
 XX Sequence 24 BP; 6 A; 5 C; 8 G; 5 T; 0 U; 0 Other;
 SQ Query Match 0.5%; Score 24; DB 2; Length 24;
 Best Local Similarity 100.0%; Pred. No. 9.8e+04;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY DB 5212 CCATGGTACCCGGATCCCGAATT 5225
 24 CCATGGTACCCGGATCCCGAATT 1
 RESULT 9
 AAA40358/C
 ID AAA40358 Standard; DNA; 28 BP.
 XX AC
 XX DT 10-NOV-2000 (first entry)
 DE pBluescriptSK+ phagemid primer SEQ ID NO: 8.
 XX Primer; cloning; ligation; ss.
 XX OS Synthetic.
 PN WO200036088-A1.
 XX PD 22-JUN-2000.
 XX PP 17-DEC-1999; 99WO-US030277.
 XX PR 17-DEC-1998; 98US-00213834.
 XX PA (ROMA/) ROMANTCHIKOV Y.
 XX PI Romanchikov Y;
 DR WPI; 2000-442381/38.
 XX Inserting a nucleic acid into a circular vector comprising joining their
 PT ends, melting, and reannealing ends at two different concentrations,
 PT useful for cloning small amounts of nucleic acids and forming genomic
 PT libraries.
 XX Example 3; Page 67; 71pp; English.
 XX This invention describes novel method (M1) for inserting a nucleic acid
 CC (N1) into a circular vector (V1) comprising joining ends of N1 and V1
 CC under a first nucleic acid concentration, melting hybridized cohesive
 CC circulation ends, and reannealing the ends at a second concentration.
 PS
 XX The methods are useful for the cloning small amounts of nucleic acids and
 CC forming genomic libraries of complex populations of DNA or cDNA. The
 CC methods allow the cloning of minute amounts of nucleic acids efficiently
 CC and avoids the size selection problems of prior art systems. Larger
 CC nucleic acid fragments are just as easily cloned, allowing highly
 CC representative libraries to be made. Vector to vector ligation is avoided
 CC using the methods. AAA0351-A40366 represents primers used to illustrate
 CC the method of the invention.
 XX Sequence 28 BP; 1 A; 1 C; 1 G; 25 T; 0 U; 0 Other;
 SQ Query Match 0.5%; Score 23.8; DB 3; Length 28;
 Best Local Similarity 92.6%; Pred. No. 1.2e+05;
 Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 5188 AACACAAANAAANAAANAAANCA 5214
 DB 28 AAAAAGAAAAAAAAGAAAAAAACTA 2
 RESULT 10
 ABN83378
 ID ABN83378 standard; DNA; 29 BP.
 XX AC ABN83378;
 XX DT 15-AUG-2002 (first entry)
 DE Mononucleotide repeat locus BAT25 probe #1.
 XX KW Mononucleotide repeat locus; human; BAT25; probe; microsatellite; tumour;
 KW ss.
 XX OS Homo sapiens.
 XX PH Key
 XX FT modified_base 29
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= 'Labelled with Fluorescein'
 XX PN EP1207210-A1.
 XX PR 22-MAY-2002.
 XX PA (HOFF) ROCHE DIAGNOSTICS GMBH.
 XX PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
 XX PR 13-NOV-2001; 2001EP-00126930.
 XX PR 15-NOV-2000; 2000EP-00124897.
 XX PI Dietmaier W;
 XX DR 2002-437469/47.
 XX WPI; 2002-437469/47.
 XX Analyzing repeat sequences in DNA using a probe which hybridizes to
 PT adjacent repetitive and non-repetitive regions and determining hybrid
 PT melting point is useful to detect microsatellite instability such as in
 PT hereditary cancer.
 XX PS Claim 16; Page 7; 19pp; English.
 XX The present invention relates to a method for analysing a target nucleic
 CC acid consisting of repetitive and non-repetitive sequences. The method
 CC comprises hybridising a polynucleotide probe comprising a segment
 CC complementary to a non-repetitive region and a segment complementary to
 CC an adjacent repetitive region, where the second segment consists of a
 CC defined number of repeats, and determining the melting point temperature
 CC of the hybrid. The method is used to analyse microsatellites, especially
 CC microsatellite instability, particularly as a means for detecting
 CC hereditary tumours. Alternatively, the method is used to identify an
 CC individual in a population. The present sequence is a probe for

CC Mononucleotide repeat locus BAT25, and was used to illustrate the invention

XX Sequence 29 BP; 26 A; 2 C; 0 G; 1 T; 0 U; 0 Other;
 SQ Query Match 0.5%; Score 23.8; DB 6; Length 29;
 Best Local Similarity 92.6%; Pred. No. 1.2e+05;
 Matches 25; Conservative 0; Mismatches 2;
 Indels 0; Gaps 0;
 OS WO959049-A1.
 Qy 518B AACAAAAAAACCA 5214
 Db 3 AAAAAGAAAATATAATATAATCA 29

RESULT_11
 ID AAX84258 standard; DNA; 25 BP.
 XX
 AC AAX84258;
 XX DT 08-SEP-1999 (first entry)
 XX DE PCR primer for human Nck associated protein 1 coding sequence.
 XX KW Nck associated protein 1; Nap1; human; apoptosis; Alzheimer's disease;
 KW therapy; PCR primer; ss.
 XX OS Synthetic.
 OS Homo sapiens.
 XX PN WO9931239-A1.
 XX PD 24-JUN-1999.
 XX PF 14-DEC-1998; 98WO-JP005646.
 XX PR 15-DEC-1997; 97JP-00363183.
 XX PA (KYOW) KYOMA HAKKO KOGYO KK.
 PA (SAKA) SAKAKI Y.
 XX PI Sakaki Y;
 XX DR WPI; 1999-395181/3.
 XX PT Protein inhibiting apoptosis, useful in the diagnosis and treatment of Alzheimer's disease.
 XX PS Example 1; Page 76; 90pp; Japanese.

XX This sequence represents a PCR primer used to isolate DNA encoding the human Nck associated protein 1 (Nap1) of the invention. Nap1 inhibits apoptosis. The protein can be used in the investigation, diagnosis and treatment (e.g. by gene therapy) of Alzheimer's disease.
 XX Sequence 25 BP; 0 A; 0 C; 1 G; 24 T; 0 U; 0 Other;
 SQ Query Match 0.4%; Score 23.4; DB 2; Length 25;
 Best Local Similarity 96.0%; Pred. No. 1.4e+05;
 Matches 24; Conservative 0; Mismatches 1;
 Indels 0; Gaps 0;

OS WO9931274-A2.
 Qy 518T CAACAAAAAAACCA 5211
 Db 25 CAAAAAAATATAATATAATCA 2

RESULT_12
 ID AAX78723 standard; DNA; 26 BP.
 XX
 AC AAX78723;
 XX DT 03-SEP-1999 (first entry)
 XX DE Human pancreatic PA153 EST-specific clone primer 12.
 XX
 CC Pancreatic disease; PA153; human; cytostatic; detection; antigen;
 CC anti-PA153; antagonist; therapy; treatment; tumour; metastasis;
 CC gene therapy; EST; expressed sequence tag; primer; ss.
 XX OS Synthetic.
 XX PN WO9931274-A2.
 XX PR 24-JUN-1999.
 XX PF 11-DEC-1998; 98WO-US026441.
 XX PR 15-DEC-1997; 97US-00990568.

XX PA (ABBO) ABBOTT LAB.
 DT

PI Billing-Medel PA; Cohen M; Colpitts TL; Friedman PN; Gordon J;
 PI Granados EN; Hodges SC; Kratochvil JD; Roberts-Rapp L;
 PI Russell JC; Stroupe SD;
 XX WPI; 1999-405041/34.

XX PA153 cDNA transcribed from pancreatic tissue.
 XX Example 2; Page 121; 123pp; English.

CC This invention describes novel contiguous and partially overlapping cDNA
 CC sequences and their encoded polypeptides, designated PA153, transcribed
 CC from human pancreatic tissue and which have cytosolic activity. The
 CC PA153 polynucleotides, proteins and antibodies are all useful in methods
 CC of detection, detection of PA153 polynucleotides, antigens or anti-PA153
 CC antibodies in samples indicative of pancreatic disease. PA153
 CC antibodies (antagonists) can also be used in vivo for therapeutic use,
 CC e.g., treatment of pancreatic disease, tumours or metastases. Antisense
 CC PA153 polynucleotides can be used in gene therapy of pancreatic diseases.
 CC AAV78712-X78725 represent primers used in the method of the invention

XX Sequence 26 BP; 0 A; 0 C; 1 G; 25 T; 0 U; 0 Other;

XX Query Match 0.4%; Score 23.4; DB 2; Length 26;
 XX Best Local Similarity 96.0%; Prd. No. 1.4e+05;
 XX Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5187 CAACAAAAAA...AAAAAA 5211
 Db 26 CAAAAAAA...AAAAAA 2

RESULT 14
 AAV71936/C
 ID AAV71936 standard; DNA; 27 BP.

XX AAV71936;
 AC 18-PFB-1999 (first entry)
 DT Anchored poly T RT-PCR primer.
 DE Normalised; cDNA library; mRNA cloning; reverse transcription;
 KW immobility; screening; hybridisation; nucleic acid amplification;
 KW expression pattern; drug development; PCR primer; RT-PCR; ss.
 XX Synthetic.
 OS WO9851789-A2.
 PN XX
 PD 19-NOV-1998.
 XX PR 13-MAY-1998; 98WO-DK000186.
 XX PR 13-MAY-1997; 97DK-00000547.
 PR 19-MAY-1997; 97US-00871030.
 PR 27-MAR-1998; 98DK-00000432.
 XX PA (DISP-) DISPLAY SYSTEMS BIOTECH APS.
 XX Wartho PR;
 PI DR; 1999-009772/01.
 XX PS Preparation of normalised, subdivided cDNA libraries from mRNA - by
 PT reverse transcription and amplification, used to screen for new genes and
 PT interacting proteins, potential drugs, and for diagnosis.

XX Example 1; Page 29; 71pp; English.
 XX The invention relates to preparation of a normalised, subdivided library
 CC of amplified cDNA from the coding regions of mRNA in a sample. The method
 CC involves reverse transcription, with at least one cDNA primer of formula
 XX

CC 5'-Gnn1-dTn2-1n3-Nnn4 to form first strand cDNA where Cnn1 = any sequence
 CC of 1-100 nucleotides; dn1 = deoxythymidine; nn1 is at least 1; n3 and n4
 CC are both 0, or n3 is 1 and n4 is at least 1; followed by second strand
 CC cDNA synthesis using the first strand as template and a second cDNA
 CC primer of a similar formula, in the presence of DNA polymerase I (or its
 CC Klenow fragment) and amplification of double-stranded cDNA with a set of
 CC amplification primers. Comparison of cDNA in the prepared library with a
 CC database (a computer-generated list of molecular weights of restricted
 CC DNA fragments of known sequence) is used to determine presence of an
 CC expressed protein in a cell, also to detect changes in such expression
 CC (particularly for diagnosis of disease). Surfaces (chip), having amplified
 CC cDNA stably immobilised on it, obtained by a similar method, are used to
 CC screen for genes of a particular family, by hybridisation with nucleic
 CC acid from the family (to identify new genes) and to detect differences in
 CC expression patterns between cells. The polypeptides expressed by the
 CC libraries can be used for drug development. Sequences AAU71935 to
 CC AAV71946 represent primers used to exemplify the method of the invention
 XX SQ Sequence 27 BP; 0 A; 1 C; 1 G; 25 T; 0 U; 0 Other;
 XX Query Match 0.4%; Score 23.4; DB 2; Length 27;
 XX Best Local Similarity 96.0%; Prd. No. 1.4e+05;
 XX Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5187 CAACAAAAAA...AAAAAA 5211
 Db 26 CAAAAAAA...AAAAAA 2

RESULT 15
 AAF74918

XX ID AAF74918 standard; DNA; 29 BP.
 AC AAF74918;
 XX DT 23-MAY-2001 (first entry)
 DE CD40L Poly-A tract sequence SEQ ID NO:15.
 XX KW Human; CD40L; promoter; CD40 ligand promoter; rheumatoid arthritis;
 KW diagnosis; antiarthritis; antirheumatic; immunosuppressive;
 KW antiinflammatory; inflammatory disease; autoimmune disease; ds.
 XX Homo sapiens.
 OS WO200119844-A1.
 XX PN WO200119844-A1.
 PD 22-MAR-2001.
 XX PR 13-SEP-2000; 2000WO-US024966.
 XX PR 13-SEP-1999; 99US-0153625P.
 XX PA (NYRE-) NEW YORK SOC RELIEF RUPTURED & CRIPPLED.
 XX DR WPI; 2001-244776/25.
 XX PT New altered CD40L promoter for use in the study, diagnosis and treatment
 PT of a variety of inflammatory disorders and autoimmune diseases, such as
 PT rheumatoid arthritis.
 XX XX Example 1; Fig 3; 90pp; English.

XX The present invention describes an isolated, purified nucleic acid, which
 CC is an altered CD40 ligand (CD40L) promoter (I) for CD40 ligand, having
 CC residues 331-455 of the sequence comprising 455 nucleotides given in
 CC AAF74905 where A in the wild type sequence at position 331 (corresponding
 CC to position -125) is replaced with C. (I) has antiarthritic,

CC antiarthritic, immunosuppressive and antiinflammatory activities, and can
 CC be used in gene therapy. (I) is useful in the study, diagnosis and
 CC treatment of inflammatory and autoimmune diseases, as well as diseases in

which elevated expression of CD40L is a factor, e.g., rheumatoid arthritis. The present sequence represents a C40L poly-A tract sequence which is used in an example from the present invention.

Search completed: September 15, 2004, 16:54:03
Job time : 1802 secs

CURRENT FILING DATE: 1998-01-14
 / EARLIER APPLICATION NUMBER: 60/035,963
 / EARLIER FILING DATE: 1997-01-27
 / EARLIER APPLICATION NUMBER: 60/035,963
 / EARLIER FILING DATE: 1997-01-27
 / EARLIER APPLICATION NUMBER: 60/064,491
 / EARLIER FILING DATE: 1997-11-16
 / NUMBER OF SEQ ID NOS: 33
 / SOFTWARE: FastSSQ for Windows Version 4.0
 / SEQ ID NO: 8
 / LENGTH: 29
 / TYPE: DNA
 / ORGANISM: Artificial Sequence
 / FEATURE:
 / OTHER INFORMATION: Translation template
 /
 Query Match 0.5%; Score 24.4; DB 3; Length 29;
 Best Local Similarity 96.2%; Pred. No. 6e+03; Indels 0; Gaps 0;
 Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 5188 AACAAACAAAAAAACCAAC 5213
 Db 4 AAAAAAAGAAAAAAACCAAC 29

RESULT 3
 / Sequence 8, Application US/09247190
 / Patent No. 6261804
 / GENERAL INFORMATION:
 / APPLICANT: Szosztak, Jack W.
 / ATTORNEY: Liu, Rine
 / TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
 / TITLE OF INVENTION: FUSIONS
 / FILE REFERENCE: 00786/53005
 / CURRENT APPLICATION NUMBER: US/09/247,190
 / EARLIER APPLICATION NUMBER: 60/035,963
 / EARLIER FILING DATE: 1997-01-21
 / EARLIER APPLICATION NUMBER: 60/064,491
 / EARLIER FILING DATE: 1997-11-06
 / EARLIER APPLICATION NUMBER: 09/007,005
 / EARLIER FILING DATE: 1998-01-14
 / NUMBER OF SEQ ID NOS: 38
 / SOFTWARE: FastSSQ for Windows Version 4.0
 / SEQ ID NO: 8
 / LENGTH: 29
 / TYPE: DNA
 / ORGANISM: Artificial Sequence
 / FEATURE:
 / OTHER INFORMATION: Translation template
 /
 Query Match 0.5%; Score 24.4; DB 3; Length 29;
 Best Local Similarity 96.2%; Pred. No. 6e+03; Indels 0; Gaps 0;
 Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 5188 AACAAACAAAAAAACCAAC 5213
 Db 4 AAAAAAAGAAAAAAACCAAC 29

RESULT 4
 US-09-244-796-8
 / Sequence 8, Application US/09244796
 / Patent No. 6261344
 / GENERAL INFORMATION:
 / APPLICANT: Szosztak, Jack W.
 / ATTORNEY: Liu, Rine
 / TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
 / FILE REFERENCE: 00786/35002
 / CURRENT APPLICATION NUMBER: US/09/244,796
 / EARLIER APPLICATION NUMBER: 60/035,963
 / EARLIER FILING DATE: 1997-01-27
 / EARLIER APPLICATION NUMBER: 60/064,491
 / EARLIER FILING DATE: 1997-11-06
 / EARLIER APPLICATION NUMBER: 09/007,005
 / EARLIER FILING DATE: 1998-01-14
 / NUMBER OF SEQ ID NOS: 33
 / SOFTWARE: FastSSQ for Windows Version 4.0
 / SEQ ID NO: 8
 / LENGTH: 29
 / TYPE: DNA
 / ORGANISM: Artificial Sequence
 / FEATURE:
 / OTHER INFORMATION: Translation template
 /
 Query Match 0.5%; Score 24.4; DB 4; Length 29;
 Best Local Similarity 96.2%; Pred. No. 6e+03; Indels 0; Gaps 0;
 Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 5188 AACAAACAAAAAAACCAAC 5213
 Db 4 AAAAAAAGAAAAAAACCAAC 29

RESULT 5
 US-09-244-796-8
 / Sequence 8, Application US/09238710A
 / Patent No. 6518018
 / GENERAL INFORMATION:
 / APPLICANT: Szosztak, Jack W.
 / ATTORNEY: Roberts, Richard W.
 / TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
 / FILE REFERENCE: 00786/35004
 / CURRENT APPLICATION NUMBER: US/09/238,710A
 / CURRENT FILING DATE: 1999-01-28
 / EARLIER APPLICATION NUMBER: 60/035,963
 / EARLIER FILING DATE: 1997-01-27
 / EARLIER APPLICATION NUMBER: 60/064,491
 / EARLIER FILING DATE: 1997-11-06
 / EARLIER APPLICATION NUMBER: 09/007,005
 / EARLIER FILING DATE: 1998-01-14
 / NUMBER OF SEQ ID NOS: 33
 / SOFTWARE: FastSSQ for Windows Version 4.0
 / SEQ ID NO: 8
 / LENGTH: 29
 / TYPE: DNA
 / ORGANISM: Artificial Sequence
 / FEATURE:
 / OTHER INFORMATION: Translation template
 /
 Query Match 0.5%; Score 24.4; DB 3; Length 29;
 Best Local Similarity 96.2%; Pred. No. 6e+03; Indels 0; Gaps 0;
 Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 5188 AACAAACAAAAAAACCAAC 5213
 Db 4 AAAAAAAGAAAAAAACCAAC 29

RESULT 6
 US-09-282-734-3
 / Sequence 3, Application US/09282734A
 / Patent No. 6537749
 / GENERAL INFORMATION:
 / APPLICANT: Robert G. Kuimelis et al.
 / TITLE OF INVENTION: ADDRESSABLE PROTEIN ARRAYS
 / FILE REFERENCE: 50036/030002

CURRENT APPLICATION NUMBER: US/09/282,734A
; CURRENT FILING DATE: 1999-03-03
; EARLIER APPLICATION NUMBER: 60/080,686
; EARLIER FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSEQ For Windows Version 3.0
; SEQ ID NO: 3
; LENGTH: 29
; TYPE: DNA
; FEATURE:
; OTHER INFORMATION: Oligonucleotide used for attaching puromycin

US-09-282-734-3

Query Match 0.5%; Score 24.4; DB 4; Length 29;
Best Local Similarity 96.2%; Pred. No. 6e+03; Mismatches 0; Indels 0; Gaps 0;
Matches 25; Conservative 0; N mismatches 1; Indels 0; Gaps 0;

Qy 5188 AACAAAGAAAAGAAAAAGAACCC 5213
Db 4 AAAAAGAAAGAAAGAAAGAAACCC 29

RESULT 7
US-08-455-627-12
; Sequence 12 Application US/08455627
; Patent No. 5571677
; GENERAL INFORMATION:
; APPLICANT: Sergei M. Gryaznov
; TITLE OF INVENTION: Convergent Synthesis of Branched and Multiply
; TITLE OF INVENTION: Connected Macromolecular Structures
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward LLP
; STREET: Five Palo Alto Square, 3000 El Camino Real
; CITY: Palo Alto
; STATE: California
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/455,627
; FILING DATE: 31-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Nakamura, Jackie N.
; REGISTRATION NUMBER: 35,966
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5000
; TELEFAX: 415-857-0663
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,627
FILING DATE: 31-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Nakamura, Jackie N.
REGISTRATION NUMBER: 35,966
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-843-5000
TELEFAX: 415-857-0663
INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:
LENGTH: 30 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA

US-08-455-627-12

Query Match 0.5%; Score 24.2; DB 1; Length 30;
Best Local Similarity 89.7%; Pred. No. 6.8e+03; Mismatches 0; Indels 3; Gaps 0;

Qy 5183 CTCTCAACAAAAAAAGAAAAAA 5211
Db 1 CACACAAAGAAAGAAAGAAAGAA 29

RESULT 8
US-08-689-856-12
; Sequence 12 Application US/08689856
; Patent No. 583058
; GENERAL INFORMATION:
; APPLICANT: Sergei M. Gryaznov
; TITLE OF INVENTION: Convergent Synthesis of Branched and Multiply
; TITLE OF INVENTION: Connected Macromolecular Structures
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward LLP
; STREET: Five Palo Alto Square, 3000 El Camino Real
; CITY: Palo Alto
; STATE: California
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/689,856
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Nakamura, Jackie N.
; REGISTRATION NUMBER: 35,966
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5000
; TELEFAX: 415-857-0663
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA

Query Match 0.5%; Score 24.2; DB 2; Length 30;
Best Local Similarity 89.7%; Pred. No. 6.8e+03; Mismatches 3; Indels 0; Gaps 0;

Qy 5183 CTCTCAACAAAAAAAGAAAAAA 5211
Db 1 CACACAAAGAAAGAAAGAAAGAA 29

RESULT 9
US-08-787-321-12
; Sequence 12 Application US/08787321A
; Patent No. 6180777
; GENERAL INFORMATION:
; APPLICANT: Roth, Thomas
; TITLE OF INVENTION: SYNTHESIS OF BRANCHED NUCLEAR ACIDS
; FILE REFERENCE: (1300)-1199 002
; CURRENT APPLICATION NUMBER: US/08/787,321A
; CURRENT FILING DATE: 1997-01-03
; EARLIER APPLICATION NUMBER: 60/009,918
; EARLIER FILING DATE: 1996-01-12
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 12
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:

OTHER INFORMATION: oligonucleotide
US-08-787-321-12

Query Match 0.5%; Score 24.2; DB 3; Length 30;
Best Local Similarity 89.7%; Pred. No. 6.8e+03; Indels 0; Gaps 0;
Matches 26; Conservative 0; Mismatches 3;

Qy 5183 CTCCTAACCAACAAAAAAAGAAAAAAA 5211
Db 1 CACRCAAAAGAAAAAAAGAAAAAAA 29

RESULT 10

US-08-566-037A-22/C
Sequence 22, Application US/0866037A
Patent No. 5756395

GENERAL INFORMATION:
APPLICANT: Haruo ONDA et al.
TITLE OF INVENTION: DNA PRIMER AND A METHOD FOR SCREENING DNAs
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wendorff, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.

ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/566,037A
FILING DATE: December 1, 1995
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:

INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 24
TYPE: Nucleic acid
STRANDEDNESS: Double
TOPOLOGY: Linear
MOLECULE TYPE: Other nucleic acid
MOLECULE TYPE: Synthetic DNA

US-08-566-037A-22

Query Match 0.5%; Score 24; DB 1; Length 24;
Best Local Similarity 100%; Pred. No. 6.7e+03; Indels 0; Gaps 0;
Matches 24; Conservative 0; Mismatches 0;

Qy 5212 CCATGGTACCCGATCTCCGATT 5235
Db 24 CCATGGTACCCGATCTCCGATT 1

RESULT 11

US-10-003-998A-7
Sequence 7, Application US/10003998A
Patent No. 664044
GENERAL INFORMATION:
APPLICANT: Roche Diagnostics GmbH

Query Match 0.4%; Score 23.4; DB 1; Length 26;
Best Local Similarity 96.0%; Pred. No. 9.9e+03; Indels 0; Gaps 0;
Matches 24; Conservative 0; Mismatches 1;

Qy 5187 CAACAAAAAAAGAAAAAAAGAAAAA 5211
Db 26 CAAAGAAAAAAAGAAAAAAAGAAAAA 2

RESULT 13
 US-09-648-040-4
 ; Sequence 4, Application US/09648040
 ; Patent No. 6436665
 ; GENERAL INFORMATION:
 ; TITLE OF INVENTION: METHODS FOR CODING AND SORTING IN VITRO
 ; FILE REFERENCE: 50036/03/2002
 ; CURRENT FILING DATE: 2000-08-25
 ; PRIOR APPLICATION NUMBER: US 6/0/151,261
 ; NUMBER OF SEQ ID NOS: 11
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 4
 ; LENGTH: 30
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Encoding molecule
 ; NAME/KEY: misc_feature
 ; LOCATION: 10
 ; OTHER INFORMATION: n at position 10 can be a, t, c, or g.
 US-09-648-040-4

Query Match 0.4%; Score 23.4; DB 4; Length 30;
 Best Local Similarity 92.3%; Pred. No. 1.1e+04;
 Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5186 TCAACAAAAAA...AAAAA 5211
 Db 26 TAAATAAAA...AAAAA 1

RESULT 14
 US-08-621-914A-1/C
 ; Sequence 1, Application US/08621914A
 ; GENERAL INFORMATION:
 ; PATENT NO. 5707807
 ; APPLICANT: KATO, KIKUYA
 ; TITLE OF INVENTION: MOLECULAR INDEXING FOR EXPRESSED GENE
 ; NUMBER OF SEQUENCES: 16
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: PENNIE & EDMONDS
 ; STREET: 1155 AVENUE OF THE AMERICAS
 ; CITY: NEW YORK
 ; STATE: NY
 ; COUNTRY: USA
 ; ZIP: 10036-2711
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC Compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patient Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/621,914A
 ; FILING DATE: 26-MAR-1996
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: LAWRENCE III, STANTON T.
 ; REGISTRATION NUMBER: 25,736
 ; REFERENCE/DOCKET NUMBER: 7005-107-999
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 790-9090
 ; TELEFAX: (212) 869-9741
 ; TELLEX: 66141 PENNIE
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 26 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: unknown

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 15, 2004, 16:24:03 ; Search time 2188 Seconds
(without alignments)

12040.701 Million cell updates/sec

Title: US-10-019-595-1

Perfect Score: 5236

Sequence: 1 cggatcgccgcggccattttggatc.....gtacccggatcttcgttgcattc 5236

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Gapop 10.0 , Gapext 1.0

Searched: 3304383 seqs, 2515761380 residues

Total number of hits satisfying chosen parameters: 1414684

Minimum DB seq length: 0

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:
1: /cgn2_6/ptodata/2/pubnra/0S07_PUBCOMB.seq;*
2: /cgn2_6/ptodata/2/pubnra/BCT_NEW_PUB.seq;*
3: /cgn2_6/ptodata/2/pubnra/US06_NEW_PUB.seq;*
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5: /cgn2_6/ptodata/2/pubnra/US07_NEW_PUB.seq;*
6: /cgn2_6/ptodata/2/pubnra/BCTUS_PUBCOMB.seq;*
7: /cgn2_6/ptodata/2/pubnra/US08_NEW_PUB.seq;*
8: /cgn2_6/ptodata/2/pubnra/PUBCOMB.seq;*
9: /cgn2_6/ptodata/2/pubnra/US09A_PUBCOMB.seq;*
10: /cgn2_6/ptodata/2/pubnra/US09B_PUBCOMB.seq;*
11: /cgn2_6/ptodata/2/pubnra/US09C_PUBCOMB.seq;*
12: /cgn2_6/ptodata/2/pubnra/US09C_NEW_PUB.seq;*
13: /cgn2_6/ptodata/2/pubnra/US09C_NEWPUB.seq;*
14: /cgn2_6/ptodata/2/pubnra/US10A_PUBCOMB.seq;*
15: /cgn2_6/ptodata/2/pubnra/US10B_PUBCOMB.seq;*
16: /cgn2_6/ptodata/2/pubnra/US10C_PUBCOMB.seq;*
17: /cgn2_6/ptodata/2/pubnra/US10C_NEW_PUB.seq;*
18: /cgn2_6/ptodata/2/pubnra/US60_NEW_PUB.seq;*
19: /cgn2_6/ptodata/2/pubnra/US60_PUBCOMB.seq;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	24.4		29	9	US-09-282-734-3	Sequence 3, Appli
2	24.4		29	10	US-09-876-2235-8	Sequence 8, Appli
3	24.4		29	15	US-10-349-6273-3	Sequence 3, Appli
4	24.4		29	17	US-10-057-7834-41	Sequence 41, Appli
C	6	23.4	0.4	26	9	US-09-099-823-14
C	7	22.8	0.4	26	9	US-09-922-914-4
C	8	22.8	0.4	26	9	US-09-922-480-7
C	9	22.8	0.4	26	9	US-09-923-246-7
C	10	22.8	0.4	26	9	US-09-922-469-7
C	11	22.8	0.4	26	17	US-10-295-723-38
C	13	22.6	0.4	26	9	US-10-659-684-38
C	14	22.6	0.4	26	9	US-09-922-480-6

ALIGNMENTS

RESULT 1
US-09-282-734-3
Sequence 3, Application US/09282734A
Publication No. US2002018297A1
GENERAL INFORMATION:
APPLICANT: Robert G. Kuimilis et al.
TITLE OF INVENTION: ADDRESSABLE PROTEIN ARRAYS
FILE REFERENCE: 5036/093002
CURRENT APPLICATION NUMBER: US/09/282,734A
CURRENT FILING DATE: 1999-03-03
EARLIER APPLICATION NUMBER: 60/080,686
EARLIER FILING DATE: 1998-04-03
NUMBER OF SEQ ID NOS: 29
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 3
LENGTH: 29
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Oligonucleotide used for attaching puromycin

RESULT 2
US-09-876-2235-8
Sequence 8, Application US/09876235
Publication No. US200302236A1
GENERAL INFORMATION:
APPLICANT: Szostak, Jack W.

APPLICANT: Roberts, Richard W.
 APPLICANT: Liu, Rine
 TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
 TITLE OF INVENTION: FUSIONS
 FILE REFERENCE: 00736/350005
 CURRENT APPLICATION NUMBER: US/09/876,235
 CURRENT FILING DATE: 2001-06-06
 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/247,190
 PRIOR FILING DATE: EARLIER FILING DATE: 1995-02-09
 PRIORITY NUMBER: EARLIER APPLICATION NUMBER: 60/035,963
 PRIORITY NUMBER: EARLIER APPLICATION NUMBER: 60/064,491
 PRIORITY NUMBER: EARLIER APPLICATION NUMBER: 60/007,005
 PRIORITY NUMBER: EARLIER APPLICATION NUMBER: 1997-11-06
 PRIORITY NUMBER: EARLIER APPLICATION NUMBER: 1998-01-14
 NUMBER OF SEQ ID NOS: 38
 SEQ ID NO: 8
 LENGTH: 29
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Translation template
 US-09-876-235-8

Query Match 0.5%; Score 24:4; DB 10; Length 29;
 Best Local Similarity 96.2%; Pred. No. 2.7e+04;
 Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5188 AACAAAGAAAAAAGAAAAAACC 5213
 Db 4 AAAAAGAAAAAAGAAAAAACC 29

RESULT 3
 US-10-348-627-3
 Sequence 3, Application US/10348627
 Publication No. US20030143616A1
 GENERAL INFORMATION:
 APPLICANT: Robert G. Kuimelis et al.
 TITLE OF INVENTION: ADDRESSABLE PROTEIN ARRAYS
 FILE REFERENCE: 50036/09002
 CURRENT APPLICATION NUMBER: US/10/348,627
 CURRENT FILING DATE: 2003-01-22
 PRIOR APPLICATION NUMBER: US/09/282,734A
 PRIOR FILING DATE: 1999-03-03
 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/080,686
 NUMBER OF SEQ ID NOS: 29
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO: 3
 LENGTH: 29
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Oligonucleotide used for attaching puromycin

US-10-348-227-3

Query Match 0.5%; Score 24:4; DB 15; Length 29;
 Best Local Similarity 96.2%; Pred. No. 2.7e+04;
 Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5188 AACAAAGAAAAAAGAAAAAACC 5213
 Db 4 AAAAAGAAAAAAGAAAAAACC 29

RESULT 4
 US-10-057-783A-41
 Sequence 41, Application US/10057783A
 Publication No. US20040091955A1
 GENERAL INFORMATION:
 APPLICANT: Forster, Anthony C.

TITLE OF INVENTION: Process and compositions for peptide, protein and
 peptide mimetic synthesis
 TITLE OF INVENTION: pepidomimetic synthesis
 FILE REFERENCE: 1
 CURRENT APPLICATION NUMBER: US/10/057,783A
 CURRENT FILING DATE: 2002-01-25
 NUMBER OF SEQ ID NOS: 48
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 41
 LENGTH: 29
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: FROM SYNTHETIC
 OTHER INFORMATION: DNA
 OTHER INFORMATION: DNA
 US-10-057-783A-41

Query Match 0.5%; Score 24:4; DB 17; Length 29;
 Best Local Similarity 96.2%; Pred. No. 2.7e+04;
 Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5188 AACAAAGAAAAAAGAAAAAACC 5213
 Db 4 AAAAAGAAAAAAGAAAAAACC 29

RESULT 5
 US-09-099-823-14/C
 Sequence 14, Application US/09099823
 Patent No. US20020189904A1
 GENERAL INFORMATION:
 APPLICANT: BILLING-MEDEL, PATRICIA
 APPLICANT: COHEN, MAURICE
 APPLICANT: COLPITTS, TRACEY L.
 APPLICANT: FRIENDMAN, PAULA N.
 APPLICANT: GORDON, JULIAN
 APPLICANT: GRANDIOS, EDWARD N.
 APPLICANT: HODGES, STEVEN C.
 APPLICANT: KLASZ, MICHAEL R.
 APPLICANT: KRATOVICH, JON D.
 APPLICANT: RUSSELL, JOHN C.
 APPLICANT: SCHERFEL, CHRISTI
 APPLICANT: STROUPE, STEPHEN D.
 APPLICANT: YU, HONG
 TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
 TITLE OF INVENTION: FOR DETECTING DISEASES OF THE BREAST
 NUMBER OF SEQUENCES: 27
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Abbott Laboratories
 STREET: 100 Abbott Park Road
 CITY: Abbott Park
 STATE: IL
 COUNTRY: USA
 ZIP: 60064-3500
 COMPUTER READABLE FORM:
 MEDIUM: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/099,823
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/879,354
 FILING DATE: 20-JUN-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Becker, Cheryl L.
 REGISTRATION NUMBER: 15,441
 REFERENCE/DOCKET NUMBER: 6120.US.P1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 847/935-1729
 TELEX: 847/938-2623
 TELEX:

```

; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base Pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-099-823-14

Query Match 0.4%; Score 23.4; DB 9; Length 26;
Best Local Similarity 96.0%; Pred. No. 4.7e+04;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Db 26 CAACAAACAAAAAAACAAAAA 2
Qy 51867 TCAACAAAAAAACAAAAAAAC 5211
Db 26 TAACAAACAAAAAAACAAAAA 1

RESULT 8
US-09-923-236-7/c
; Sequence 7, Application US/09923236
; Patent No. US0020090677A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; ATTORNEY: Adler, David A.
; TITLE OF INVENTION: SECRETED SALIVARY ZSIG63 POLYPEPTIDE
; FILE REFERENCE: 97-71
; CURRENT APPLICATION NUMBER: US/09/923,236
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/124,820
; PRIOR FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO: 7
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE: FEATUR
; OTHER INFORMATION: Oligonucleotide primer ZC7764a
; US-09-923-236-7

Query Match 0.4%; Score 22.8; DB 9; Length 26;
Best Local Similarity 92.3%; Pred. No. 6.8e+04;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Db 26 TAACAAACAAAAAAACAAAAA 1

RESULT 9
US-09-923-246-38/c
; Sequence 38, Application US/09923246
; Patent No. US20020128446A1
; GENERAL INFORMATION:
; APPLICANT: NC. US20020128446A1
; ATTORNEY: Presenell, Scott R.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHAI1 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/09/923,246
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US /09/522,217
; PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,013
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO: 38
; LENGTH: 26

Query Match 0.4%; Score 23.4; DB 15; Length 30;
Best Local Similarity 92.3%; Pred. No. 5.3e+04;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Db 5 AAAANAAAACAAAAAAAC 30
Qy 5188 AACAAACAAAAAAAC 5213
Db 5 AAAANAAAACAAAAAAAC 30

RESULT 7
US-09-922-4.80-7/c
; Sequence 7, Application US/09922480
; Patent No. US20020081701A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; ATTORNEY: Adler, David A.
; TITLE OF INVENTION: SECRETED SALIVARY ZSIG63 POLYPEPTIDE
; FILE REFERENCE: 97-71
; CURRENT APPLICATION NUMBER: US/09/922,480
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/124,820
; PRIOR FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO: 7
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

```


; TITLE OF INVENTION: SECRETED SALIVARY ZSIG63 POLYPEPTIDE
 ; FILE REFERENCE: 97-71
 ; CURRENT APPLICATION NUMBER: US/09/922,480
 ; CURRENT FILING DATE: 2001-08-03
 ; PRIOR APPLICATION NUMBER: US 60/124,820
 ; PRIOR FILING DATE: 1999-03-17
 ; NUMBER OF SEQ ID NOS: 9
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO: 6
 ; LENGTH: 26
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE: OTHER INFORMATION: Oligonucleotide primer ZC7231
 US-09-922-469-6

Query Match 0.4% Score 22.6; DB 9; Length 26;
 Best Local Similarity 92.0%; Pred. No. 7.7e+01; Indels 0; Gaps 0;
 Matches 23; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 5187 CAACAAAAAAAGAAAAAAA 5211
 Db 26 BAAAAAAAAGAAAAAAA 2

RESULT 14
 US-09-922-236-6/c
 ; Sequence 6, Application US/09923236
 ; Patent No. US20020050677A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Sheppard, Paul O.
 ; TITLE OF INVENTION: SECRETED SALIVARY ZSIG63 POLYPEPTIDE
 ; FILE REFERENCE: 97-71
 ; CURRENT APPLICATION NUMBER: US/09/923,236
 ; CURRENT FILING DATE: 2001-08-03
 ; PRIOR APPLICATION NUMBER: US 60/124,820
 ; PRIOR FILING DATE: 1999-03-17
 ; NUMBER OF SEQ ID NOS: 9
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO: 6
 ; LENGTH: 26
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Oligonucleotide primer ZC7231
 US-09-922-236-6

Query Match 0.4% Score 22.6; DB 9; Length 26;
 Best Local Similarity 92.0%; Pred. No. 7.7e+01; Indels 0; Gaps 0;
 Matches 23; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 5187 CAACAAAAAAAGAAAAAAA 5211
 Db 26 BAAAAAAAAGAAAAAAA 2

RESULT 15
 US-09-922-469-6/c
 ; Sequence 6, Application US/09922469
 ; Patent No. US2002017027A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Sheppard, Paul O.
 ; TITLE OF INVENTION: SECRETED SALIVARY ZSIG63 POLYPEPTIDE
 ; FILE REFERENCE: 97-71
 ; CURRENT APPLICATION NUMBER: US/09/922,469
 ; CURRENT FILING DATE: 2001-08-03
 ; PRIOR APPLICATION NUMBER: US 60/124,820
 ; PRIOR FILING DATE: 1999-03-17
 ; NUMBER OF SEQ ID NOS: 9
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO: 6

; LENGTH: 26
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Oligonucleotide primer ZC7231
 US-09-922-469-6

Search completed: September 16, 2004, 02:22:36
 Job time : 2119 secs

Qy 5187 CAACAAAAAAAGAAAAAAA 5211
 Db 26 BAAAAAAAAGAAAAAAA 2

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Result No.	Score	Query	Match	Length	DB ID	Description
c 1	24.4	AZ481286/	AZ481286	28	AZ481286	28 bp DNA linear library Mus musculus genomic sequence.
c 2	24.4	0.5	29	14	CF28476	NACI--03-N
c 3	24.4	0.5	29	14	CF28476	N33150 YY06301_S1
c 4	24.4	0.5	30	28	AZ485624	CF296851 1M0313H11
						N52529 YV335A12_S1
						AL587582 AL587582
						CF299294 7LEAF--03
						BQ590537 E012843-0
						CA953764 B12A03_se
						CF312319 ABF--07-P
						CG762637 1119089E1
						T52836 Ya81b09_S1
						CF299716 7LEAF--03
						A1038686 Homo sapi
						CF337410 JMT--07_N
						R3797 YF50C03_S1
						A2492630 1M0326B22
						BGB6551 602783643
						AZ962183 2N0230124
						BX670391 DRNAFA06
						BX554611 BX54611
						CF276855 14BTI--02
						CR301561 7LEAF--02
						CF301561 HD--11-O1
						AZ386491 1M0145D02
						AZ390642 1M0152H07
						AZ44871 1M0173U14
						AZ459280 1M0264A05
						AZ644621 1M0508F12
						AZ78625 2N0031H12
						AZ834990 2M0129A05
						AZ970038 2M0243J02
						AZ984490 2M0226H05
						AZ993423 2M0278C19
						AI478922 T. brucei
						AI453584 T. brucei
						AI494439 T. brucei
						AI495622 T. brucei
						Unpublished (2000)
						Contact: Robert B. Weiss
						University of Utah Genome Center
						University of Utah
						Rm. 302, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
						84112, USA
						Tel: 801 585 5606
						Fax: 801 585 7177

ALIGNMENTS

RESULT 1
AZ481286/

LOCUS IM0303L24F Mouse 10kb plasmid JUGCM library Mus musculus genomic sequence.

DEFINITION Clone JUGCM0303L24 F, genomic survey sequence.

ACCESSION AZ481286

VERSION AZ481286.1 GI:10642351

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Murinae; Mus.

REFERENCE Dunn,D., Aoyagi,A., Barber,M., Beacon,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meiner,E., Pedersen,T., Peilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhäusern,A., and Wright,D.,Weiss,R.

AUTHORS

TITLE Mouse whole genome scaffolding with paired end reads from 10kb

JOURNAL Unpublished (2000)

COMMENT

Dunn,D., Aoyagi,A., Barber,M., Beacon,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meiner,E., Pedersen,T., Peilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhäusern,A., and Wright,D.,Weiss,R.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
c 1	24.4	AZ481286	AZ481286	28	AZ481286	28 bp DNA linear library Mus musculus genomic sequence.
c 2	24.4	0.5	29	14	CF28476	NACI--03-N
c 3	24.4	0.5	29	14	CF28476	N33150 YY06301_S1
c 4	24	0.5	30	28	AZ485624	CF296851 1M0313H11
						N52529 YV335A12_S1
						AL587582 AL587582
						CF299294 7LEAF--03
						BQ590537 E012843-0
						CA953764 B12A03_se
						CF312319 ABF--07-P
						CG762637 1119089E1
						T52836 Ya81b09_S1
						CF299716 7LEAF--03
						A1038686 Homo sapi
						CF337410 JMT--07_N
						R3797 YF50C03_S1
						A2492630 1M0326B22
						BGB6551 602783643
						AZ962183 2N0230124
						BX670391 DRNAFA06
						BX554611 BX54611
						CF276855 14BTI--02
						CR301561 7LEAF--02
						CF301561 HD--11-O1
						AZ386491 1M0145D02
						AZ390642 1M0152H07
						AZ44871 1M0173U14
						AZ459280 1M0264A05
						AZ644621 1M0508F12
						AZ78625 2N0031H12
						AZ834990 2M0129A05
						AZ970038 2M0243J02
						AZ984490 2M0226H05
						AZ993423 2M0278C19
						AI478922 T. brucei
						AI453584 T. brucei
						AI494439 T. brucei
						AI495622 T. brucei

Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0303 Row: L Column: 24
 Seq primer: CGTGTGAAACCCAGGCCGT
 Class: Plasmid ends

FEATURES Location/Qualifiers

High quality sequence stop: 28.

source

1..28
 /organism="Mus musculus"
 /mol type="Genomic DNA"
 /stran="C57BL/6J"
 /db_xref="taxon:10090"
 /clones="UGCIM03031L24"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb Plasmid UGCIM library"
 /note="Vector: PWD4env; Purified Genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnarefs/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA Polymerase and T4
 polynucleotide kinase. Adaptor Oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pW42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptored mouse DNA was annealed to
 adaptored vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

ORIGIN

Query Match 0.5%; Score 24.4; DB 28; Length 28;
 Best Local Similarity 96.2%; Pred. No. 1.6e+07;
 Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5187 CAACAAAAA.....AAC 5212
 Db 28 CAACAAAAA.....AAC 3

RESULT 3
 AZ819924

LOCUS AZ819924

DEFINITION 2M0091A19R Mouse 10kb Plasmid UGCIM library Mus musculus genomic

CLONE UGCIM031L24 R, genomic survey sequence.

ACCESSION AZ819924

VERSION AZ819924.1 GI:12999832

KWDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Metazoa; Eutheria; Chordata; Craniata; Vertebrata; Buteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathii; Murinae; Murinae; Mus.

REFERENCE 1 (bases 1 to 29)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islami,H., Niederauer,A. and Wright,D., Weiss,R., Tingey,A., von
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederauer,A. and Wright,D., Weiss,R.,

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center

DEFINITION 07-MAR-1995

LOCUS T67079 mRNA linear

DEFINITION Ya52:07.r3 Soares fetal liver spleen INFEL Homo sapiens cDNA clone
 IMAGE:6:6555:5, similar to gb:X02492 INTERFERON-INDUCED PROTEIN 6-16

PREREOSOR (HUMAN); mRNA sequence.

ACCESSION T67079

VERSION T67079.1 GI:6766519

EST

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens (human)

ORGANISM Eukaryota; Metazoa; Chordata; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 29)

AUTHORS Hillier,L., Clark,N., Dubucque,T., Elliston,K., Hawkins,M.,
 Holman,M., Holtzman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
 Parsons,J., Rafkin,L., Rohlfing,T., Soares,M., Tan,F.,
 Trevisakis,E., Waterston,R., Williamson,A., Wohldmann,P. and
 Wilson,R.

TITLE The WashU-Merck EST Project

JOURNAL Unpublished (1995)

COMMENT Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 261 1810
 Email: est@watson.wustl.edu

FEATURES Location/Qualifiers

source

1..29

High quality sequence starts: 1

High quality sequence stops: 1

Source: IMAGE Consortium, LInL
 This clone is available royalty-free through LInL; contact the
 IMAGE Consortium (Info@image.lnl.gov) for further information.

Trace consider overall poor quality

Seq primer: T7

High quality sequence stop: 1.

FEATURES Location/Qualifiers

source

1..29

/organism="Homo sapiens"
 /clone lib="Soares fetal liver spleen INFEL"
 /note="Organ: Liver and Spleen; Vector: PT73D (Pharmacia)
 with a modified polylinker; Site 1: Pac I; Site 2: Eco RI;
 1st strand cDNA was primed with a Pac I - oligo(dT) primer
 [5', AACCTGGAGATAATTAAGCATTTTTTTTTTTTTTTTT 3'],
 double-stranded cDNA was ligated to Eco RI adaptors
 (Pharmacia), digested with Pac I and cloned into the Pac I
 and Eco RI sites of the modified PT73D vector. Library
 went through one round of normalization. Library
 constructed by Bento Soares and M.Fatima Bonaldo."

Query Match 0.5%; Score 24.4; DB 14; Length 29;
 Best Local Similarity 92.6%; Pred. No. 1.6e+07;
 Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5184 TCCTCAACAAAAA.....AAAAAAA 5210
 Db 3 TCCTCAACAAAAA.....AAAAAAA 29

RESULT 3
 AZ819924

LOCUS AZ819924

DEFINITION 2M0091A19R Mouse 10kb Plasmid UGCIM library Mus musculus genomic

CLONE UGCIM031L24 R, genomic survey sequence.

ACCESSION AZ819924

VERSION AZ819924.1 GI:12999832

KWDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathii; Murinae; Murinae; Mus.

REFERENCE 1 (bases 1 to 29)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islami,H., Niederauer,A. and Wright,D., Weiss,R.,

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center

DEFINITION 07-MAR-1995

LOCUS T67079 mRNA linear

DEFINITION Ya52:07.r3 Soares fetal liver spleen INFEL Homo sapiens cDNA clone
 IMAGE:6:6555:5, similar to gb:X02492 INTERFERON-INDUCED PROTEIN 6-16

PREREOSOR (HUMAN); mRNA sequence.

ACCESSION T67079

VERSION T67079.1 GI:6766519

EST

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens (human)

ORGANISM Eukaryota; Metazoa; Chordata; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 29)

AUTHORS Hillier,L., Clark,N., Dubucque,T., Elliston,K., Hawkins,M.,
 Holman,M., Holtzman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
 Parsons,J., Rafkin,L., Rohlfing,T., Soares,M., Tan,F.,
 Trevisakis,E., Waterston,R., Williamson,A., Wohldmann,P. and
 Wilson,R.

TITLE The WashU-Merck EST Project

JOURNAL Unpublished (1995)

COMMENT Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 261 1810
 Email: est@watson.wustl.edu

FEATURES Location/Qualifiers

source

1..29

/organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="Taxon:10090"
 /clone="UUGCIM0261124"
 /sex="Male"
 /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UGGCIM library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (<http://www.jax.org/resources/documents/dnare/>). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA Polymerase and T4
 Polynucleotide kinase. Adapter oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adapter DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (gi:4722114 gb:AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adapter mouse DNA was annealed to
 adapter DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

ORIGIN

Query Match	0.5%	Score 24.4;	DB 28;	Length 30;
Best Local Similarity	96.2%	Pred. No. 1.6e+07;		
Matches	25;	Conservative	0;	Mismatches 0;
Indels	0;	Gaps 0;		
Qy	5188 AACAAAAAA.....AAC 5213			
Db	: 3 AAAA.....AAA.....AAC 28			

RESULT 4
 AZ458127/C 30 bp DNA linear GSS 04-OCT-2000
 LOCUS IM0261124R Mouse 10kb plasmid UGGCIM library Mus musculus genomic
 DEFINITION clone UUGCIM0261124 R, genomic survey sequence.

ACCESSION	AZ458127
VERSION	AZ458127.1
KEYWORDS	GI:10616252
SOURCE	Mus musculus (house mouse)
ORGANISM	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Murinae; Mus.
REFERENCE	1 (bases 1 to 30)
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Maimoud,M., Meenin,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb Plasmid inserts Unpublished (2000)
JOURNAL	Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00
COMMENT	Plate: 0261 Row: I Column: 24 Seq primer: CGTTAAGACGCCCCAGT Class: Plasmid ends High quality sequence stop: 30.
FEATURES	Location/Qualifiers 1. .30 Source

RESULT 5
 AZ809971/C 28 bp DNA linear GSS 20-FEB-2001
 LOCUS 2K0074C14F Mouse 10kb plasmid UGGCIM library Mus musculus genomic
 DEFINITION clone UGC2N0074C14 F, Genomic survey sequence.

ACCESSION	AZ809971
VERSION	AZ809971.1
KEYWORDS	GI:12976769
SOURCE	Mus musculus (house mouse)
ORGANISM	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Murinae; Mus.
REFERENCE	1 (bases 1 to 28)
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Maimoud,M., Meenin,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb Plasmid inserts Unpublished (2000)
JOURNAL	Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00
COMMENT	Plate: 0074 Row: C Column: 14 Seq primer: CGTTAAGACGCCCCAGT Class: Plasmid ends High quality sequence stop: 28.
FEATURES	Location/Qualifiers 1. .28 Source

/organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="Jaxon:10090"
 /clone="UJGCD2M0074C14"
 /sex="Male"
 /lab_host="E. Coli strain XL1-Gold, Ti-resistant, F-"
 /clone_lab="Mouse 10kb Plasmid UGCGM library"
 /note="Vector: PCR4TOPO; Site 1: EcoRI; mRNA was capped with Oligoribonucleotides and then used as templates for RT-PCR."

ORIGIN

Query Match	0.5%	Score 23.8;	DB 14;	Length 29;
Best Local Similarity	92.6%	Pred. No. 2e+07;	0;	Caps 0;
Matches	25;	Conservative	2;	Indels 0;
Qy	5188 AACAAATAAAAAATAAAAAACCA 5214			
Db	1 AAAAAAATAAAAAATAAAAAACAA 27			

RESULT 7
 N33150/C
 LOCUS N33150_51 Soares melanocyte 2NbEM Homo sapiens cDNA clone.
 DEFINITION IMAGE:70480 3, similar to gb:D29805 N-ACETILLACTOSAMINE SYNTHASE (HUMAN); mRNA sequence.
 ACCESSION N33150
 VERSION N33150_1
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCES
 AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rikkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P., and Wilson,R.
 TITLE The WashU-Merck EST Project
 JOURNAL Unpublished (1995)
 COMMENT Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 High quality sequence starts: 1
 Source: IMAGE Consortium, LiNU. This clone is available royalty-free through LiNU; contact the IMAGE Consortium (info@image.lnl.gov) for further information.
 Trace considered overall poor quality
 Seq primer: m13 -40 forward
 High quality sequence stop: 1.
 Location/Qualifiers
 1..25
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="NCBI:3880122"
 /db_xref="Taxon:9606"
 /clone="IMAGE:70480_1"
 /sex="Male"
 /tissue_type="melanocyte"
 /lab_host="DH10B (ampicillin resistant)"
 /clone_lab="Soares melanocyte 2NbEM"
 /note="Vector: pT7T3D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dt) primer [5, TGTTCACCTGAGTGGAGTGGAGGCCGAATGTTTTTTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library constructed by Bento Soares and M. Patima Bonaldo. RNA from normal foreskin melanocytes (FS374) was kindly provided by Dr. Anthony P. Albino."

ORIGIN

/organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="Jaxon:10090"
 /clone="UJGCD2M0074C14"
 /sex="Male"
 /lab_host="E. Coli strain XL1-Gold, Ti-resistant, F-"
 /clone_lab="Mouse 10kb Plasmid UGCGM library"
 /note="Vector: PCR4TOPO; Site 1: EcoRI; mRNA was capped with Oligoribonucleotides and then used as templates for RT-PCR."

ORIGIN

/organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="Taxon:4530"
 /clone="NaCl--03-G12"
 /tissue_type="callus"
 /dev_stage="proliferated callus on 2N6 media for 30 days"
 /lab_host="E.coli DH10B"

Query Match 0.4%; Score 23.4; DB 14; Length 25;
 Best Local Similarity 96.0%; Pred. No. 2.4e+07; Indels 0; Gaps 0;
 Matches 24; Conservative 0; Mismatches 1; JOURNAL
 QY 5188 AACAAAAAAAGAAC 5212
 Db 25 AAAAAGAAAAAAAGAAC 1

RESULT 8
 CP296851/C
 LOCUS DEFINITION CP296851-07-G13.b1 Rice leaf plasmid cDNA library I (30DGs) Oryza sativa cDNA clone 30DGs--07-G13, mRNA sequence.

ACCESSION CP296851
 VERSION CP296851.1
 KEYWORDS EST
 SOURCE Oryza sativa
 ORGANISM Eukaryota; Viridiplantae; Streptophytina; Embryophyta; Tracheophyta; Spermatophytina; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
 REFERENCE 1 (bases 1 to 26)
 AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K., and Nahm, B.H.
 TITLE Large-scale Sequencing Analysis of Rice ESTs
 COMMENT Unpublished (2003)
 Contact: Nahm, B. H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Biosciences and Bioinformatics, Myongji University
 Yongin, Kyonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahn@gbbio.com, bhnahn@bio.myongji.ac.kr.

FEATURES source
 Location/Qualifiers
 1..26 "Oryza sativa"
 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:45301"
 /clone="30DGs--07-G13"
 /tissue_type="leaf"
 /dev_stage="30 days after germination"
 /lab_host="E. coli DH10B"
 /clone_lib="Rice leaf Plasmid cDNA library I (30DGs)"
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

ORIGIN
 Query Match 0.4%; Score 23.4; DB 14; Length 26;
 Best Local Similarity 96.0%; Pred. No. 2.4e+07; Indels 0; Gaps 0;
 Matches 24; Conservative 0; Mismatches 1; JOURNAL
 QY 5188 AACAAAAAAAGAAC 5212
 Db 25 AAAAAGAAAAAAAGAAC 1

RESULT 9
 AZ485624
 LOCUS DEFINITION 1N013H1F Mouse 10kb plasmid UGCM library Mus musculus genomic clone UGCM0313H1 F, genomic survey sequence.
 ACCESSION A2485624
 VERSION A2485624.1 GI:10651605
 KEYWORDS GSS
 SOURCE Mus musculus (house mouse)
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurgnathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 26)
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H.; Longacre, S.; Mahmoud, M.; Meenen, B.; Pedersen, T., Reilly, M.; Rose, M.; Rose, R.; Stokes, R.; Tingey, A.; von Niederauer, A.; and Wright, D.; Weiss, R.; Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 305, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0313 Row: H column: 11
 Seq primer: CGTTTAAACGAGCCAGT
 Class: plasmid ends
 High Quality sequence stop: 26.
 Location/Qualifiers
 1..26
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGCM0313H1"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Ti-resistant, F-"
 /clone_lib="Mouse 10kb Plasmid UGCM library"
 /note="Vector: pW42zny; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.Jax.org/resources/documents/dnarec/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114.gb|AF129072.1) a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptorized mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

FEATURES source
 Location/Qualifiers
 1..26 "Oryza sativa"
 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:45301"
 /clone="30DGs--07-G13"
 /tissue_type="leaf"
 /dev_stage="30 days after germination"
 /lab_host="E. coli DH10B"
 /clone_lib="Rice leaf Plasmid cDNA library I (30DGs)"
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

ORIGIN
 Query Match 0.4%; Score 23.4; DB 28; Length 26;
 Best Local Similarity 96.0%; Pred. No. 2.4e+07; Indels 0; Gaps 0;
 Matches 24; Conservative 0; Mismatches 1; JOURNAL
 QY 5191 AAAAAGAAAAAAAGAAC 5215
 Db 1 AAAAAGAAAAAAAGAAC 25

RESULT 10
 N52529/C
 LOCUS DEFINITION YY3-12..1 Scores fetal liver spleen INFILS Homo sapiens mRNA linear EST 15-FEB-1996 IMAGE:244702.3, similar to 9b:X68242 PUTATIVE HIV-1 INDUCED PROTEIN HIN-1 (HUMAN); mRNA sequence.
 ACCESSION N52529
 VERSION N52529.1 GI:1193695
 KEYWORDS EST
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarinini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 27)

AUTHORS	Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hullman,M., Kucaba,T., Le M., Lennon,G., Marra,M., Parsons,J., Rieffin,L., Rohlfing,T., Scores,M., Tan,F., Terasakis,E., Watersson,R., Williamson,A., Wohldmann,P. and Wilson,R.	FEATURES	source	Query Match Score 23.4%; Best Local Similarity 92.3%; Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
JOURNAL	The WashU-Merck EST Project	Location/Qualifiers	1..28	/organism="Gallus gallus" /mol_type="mRNA" /db_xref="taxon:9031" /clone="ROS059D03" /tissue_type="Unknown" /lab_host="DH10B"
COMMENT	Contact: Wilson RK 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: estwation.wustl.edu This clone is available royalty-free through LInL; contact the IMAGE Consortium (info@image.lnl.gov) for further information. Trace Considered over/1 Poor Quality Seq primer: m13 -40 forward High quality sequence stop: 1.	Location/Qualifiers	1..27	/organism="Homo sapiens" /mol_type="mRNA" /db_xref="GDB:373948" /clone="IMAGE:244702" /sex="male" /dev_stage="20 week-post conception fetus" /lab_host="DH10B (ampicillin resistant)" /clone lib="Soares fetal liver spleen 1NFLS" /note="Organ: Liver and spleen; Vector: pRT3D (Pharmacia) with a modified Polylinker; Site 1: Pac I; Site 2: Eco RI; 1st strand cDNA was primed with a Pac I - oligo(Tdr) Primer [5'-AATCTGGAAATAAAGATCTTTTGTTCCTT 3]; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pRT3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."
FEATURES	source	Query Match Score 23.4%; Best Local Similarity 92.3%; Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	1..28	/organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9031" /clone="ROS059D03" /tissue_type="Unknown" /lab_host="DH10B"
RESULTS	AL587582/C	DEFINITION	AL587582 BP Chicken Brain mRNA sequence.	Query Match Score 23.4%; Best Local Similarity 92.3%; Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
ACCESSION	AL587582	VERSION	GI:13112616	Query Match Score 23.4%; Best Local Similarity 92.3%; Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
KEYWORDS	EST.	ORGANISM	Gallus gallus (chicken)	Query Match Score 23.4%; Best Local Similarity 92.3%; Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
REFERENCE	1..28	ORGANISM	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Phasianinae; Gallus.	Query Match Score 23.4%; Best Local Similarity 92.3%; Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
AUTHORS	Murray,F.	TITLE	BP Chicken Brain Library	Query Match Score 23.4%; Best Local Similarity 96.0%; Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
JOURNAL	Unpublished (2001)	COMMENT	Contact: Frazer Murray Dept. Genomics and Bioinformatics Roslin Institute Roslin, Midlothian, EH25 9PS, UK Tel: +44 (0)131 527 4200 Fax: +44 (0)131 440 0434 Email: frazer.murray@bsrc.ac.uk	Query Match Score 23.4%; Best Local Similarity 96.0%; Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	5188 AACAAAAA.....AAC	5212	DEFINITION	B12A03 seq cDNA Peking library 12hr SCN3 Glycine max cDNA clone
DB1 AAA.....AAAAA.....AAC	25	ACCESSION	B12A03 5', mRNA sequence.
RESULT	13	LOCUS	CA853744	VERSION
	BQ590537/c	29 bp	DEFINITION	CA853744.1 GI:13390569
	EST	mRNA	KEYWORDS	EST.
	BQ590537	linear	SOURCE	Glycine max (soybean)
ACCESSION	BQ590537	MPIZ-ADIS-024-019-C03-T7	ORGANISM	Glycine max
KEYWORDS	CDNA clone	3-PRIME, mRNA sequence.	REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
SOURCE	Beta vulgaris	EST.	AUTHORS	Eukaryota; Magnoliophyta; eudicots; core eudicots;
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	EST.	TITLE	Spermatophyta; Fabaceae; Papilionoideae; Phaseoleae;
	Spermatoophyta; Magnoliophyta; eudicotyledons; core eudicots;	COMMENT	JOURNAL	Glycine max
	Caryophyllales; Amaranthaceae; Beta.	1 (bases 1 to 29)	COMMENT	1 (bases 1 to 24)
REFERENCE	Herrwig, R.; Schulz, B.; Weissaar, B.; Henning, S.; Steinfath, M., Drungowski, M., Stahn, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H.	1 (bases 1 to 29)	CONTACT	Alkharouf, N.W.
AUTHORS	and Radefeld, U.	EST.	US Department of Agriculture (USDA), ARS, PSI	Soybean Genomics and Improvement Laboratory (SGIL)
	Construction of a 'unigene' cDNA clone set by oligonucleotide	EST.	Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,	Unpublished (2002)
	fingerprinting allows access to 25 000 potential sugar beet genes	COMMENT	USA	Contact: Alkharouf, N.W.
	Plant J. 32 (5), 845-857 (2002)	FEATURES	Tel: 301 504 5750	Soybean Genomics and Improvement Laboratory (SGIL)
	22362189	source	Fax: 301 504 5758	US Department of Agriculture (USDA), ARS, PSI
JOURNAL	12472698	organism="Glycine max"	Email: alkharouf@ars.usda.gov.	Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,
MEDLINE		/molType="mRNA"	Location/Qualifiers	1. 24
PUBMED		/cultivar="Peking"		2. 24
COMMENT	Contact: Weissaar B	/db_xref="taxon:3847"		3. 24
	Max-Planck-Institute for Plant Breeding Research	/clone="B12A03"		4. 24
	Carl-von-Linné Weg 10, 50829 Koeln, Germany	/tissue_type="Roots"		5. 24
	Fax: 0049215022851	/dev_stage="Seedlings"		6. 24
	Email: weissaar@mpiz-koeln.mpg.de	/clone_lib="cDNA Peking library 12hr SCN3"		7. 24
	Insert Length: 29	/notes=Vector: pBluecript SK-		8. 24
	Std Error: 0.00	/CDNA Clones from mRNA		9. 24
	Plate: 19 row: C column: 03	extracted from roots of soybean cv. Peking 12 hrs after		10. 24
	Seq Primer: T7: GTATACTGACTCACTATAGGGC.	infection by SCN race 3. These are cloned in pBluecript		11. 24
FEATURES	Location/Qualifiers	SK- phagemid."		12. 24
source	1. 29	ORIGIN		13. 24
	/organism="Beta vulgaris"	Query Match		14. 24
	/molType="mRNA"	Best Local Similarity		15. 24
	/cultivar="KWS2320	100.0%		16. 24
	(double haploid, monogerm breeding	Prd: 0; Mi: 0		17. 24
	line)"	Matches 23; Conservative 0; Mi: 0		18. 24
	/db_xref="GABI:189579"	Indels 0; Gaps 0;		19. 24
	/db_xref="taxon:16194"	Organism		20. 24
	/clone="024-019-C03"	CF312319/c		21. 24
	/tissue_type="storage root"	CF312319		22. 24
	/lab_host="EMDH10"	CF312319 ABF3-overexpressing transgenic rice		23. 24
	/clone_lib="MPIZ-ADIS-024-storage root"	plasmid cDNA		24. 24
	/note=Vector: PCMVSPORT6; Site1: Salt; Site2: NotI;	library Note: SCN		25. 24
	CDNA 1 library from sugar beet, Library provided by KWS	EST 15-AUG-2003		26. 24
	Kleinwanzleben Saatzaehn AG Einbeck, Germany, contact:	LOCUS		27. 24
	b.schulz@kws.de; cloning sites Salt-NotI, primer sites and	DEFINITION		28. 24
	orientation:	Accession		29. 24
	SP6-Salt-CAACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7;	VERSION		30. 24
	Note: sequencing granted in the context of the GABI-Beet	JOURNAL		31. 24
	Project, local PI: Dr. Katharina Schneider, coordinator:	COMMENT		32. 24
	Prof. Christian Jung, Sequence submission managed by	CONTACT		33. 24
	RZPD/GABI-primary database: http://gabi.rzpd.de"	Genomics and Genetics Institute, GreenGene Biotech Inc.; Division		34. 24
ORIGIN		of Bioscience and Bioinformatics, MyongJi University		35. 24
		Yongin, Kyeonggi, Korea		36. 24
		Tel: 82 31 330 6193		37. 24
		Fax: 82 31 321 6355		38. 24
Query Match	0.4%	Score 23.4; DB 13;	Length 29;	
Best Local Similarity	96.0%	Prd: No. 2, 3e+07;		
Matches 24;	Conservative 0;	Mismatches 1;	Indels 0;	
		Gaps 0;		
QY	5187 CAACRAAAA.....AAAAA	5211	REFERENCE	1 (bases 1 to 24)
DB	28 CAA.....AAAAA.....AAA	4	AUTHORS	Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
RESULT	14		Song, S.I., Kim, J.K., Kim, J.-K. and Nahm, B.H.	
CA853764/C			TITLE	Large-scale Sequencing Analysis of Rice ESTs
LOCUS			JOURNAL	Unpublished (2003)
			COMMENT	Contact: Nahm, B.H.
				Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
				of Bioscience and Bioinformatics, MyongJi University
				Yongin, Kyeonggi, Korea
				Tel: 82 31 330 6193
				Fax: 82 31 321 6355

FEATURES Email: bhnahn@ggbio.com, bhnahn@bio.myongji.ac.kr.
 source Location/Qualifiers
 1..24
 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nachdong"
 /db_xref="Taxon:4530"
 /clone="ABF-07-P12"
 /tissue_type="Leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="ABP3-overexpressing transgenic rice plasmid
 cDNA library (ABP)"
 /note="Vector: PCR4 TOPO; Site_1: EcoRI; Leaf was dried
 for 2hrs. Oligo-capped mRNA was reverse transcribed and
 then used for PCR. mRNA was prepared from ABA-responsive
 element binding transcription factor 3 overexpression
 line."

ORIGIN

Query Match 0.4%; Score 23; DB 14; Length 24;
 Best Local Similarity 100.0%; Pred. No. 2.8e+07;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 • Qy 5191 AAAAAAAACCAAAACCAAC 5213
 Db 23 AAAAAAAACCAAAACCAAC 1

Search completed: September 16, 2004, 01:40:37
 Job time : 12085 secs